

SEQUENCE PROTOCOL

<110> Degussa-Hüls AG, Forschungszentrum Jülich GmbH

<120> New nucleotide sequences which code for the fadD15 gene

<130> 0000011 BT

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<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (247)..(2103)

<223> fadD15

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<221> -10_signal

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<222> (72)..(78)

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taagaagtta ttgacacact gaatacatag agaaaaattc catgtgggta aagatatgcc 180
taaagatctg accaaaaacg tgactaaaga cgtgacgaca caagtacagc caaattaaag 240
gaaagg ttg aat ttg acc atg act tca cct aat acc ctg cag gaa tac      288
      Leu Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr
        1             5             10

act gaa cct gcc aag tac acc atc gga gaa tct gaa acc tgc ctg acc      336
Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr
  15             20             25             30

gcc ctt cta gat cag att aag act cga cct tac gga gtt ttg ttc agc      384
Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser
      35             40             45

aag cct gcc aac tat gag tgg gtg aat gta act gcc aaa gaa ttt cag      432
Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln
      50             55             60

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Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu	
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cag gga gac cgt gtc gcg ctg ctg tcc aat act cgc tat gag tgg gct	528
Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala	
80 85 90	
gtg ctt gat ttc gct atc tgg gcc gct ggc gca gtg agc gtg cct atc	576
Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile	
95 100 105 110	
tac agc tcc tct tca ctg tcc caa att gag tgg atc att gag gat tcc	624
Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser	
115 120 125	
ggc gct gtt ttg gcc att acc gaa acc cct gat cat acc gac ttg atg	672
Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met	
130 135 140	
aag aac ctg gtc atc ggt gaa gac gga act cca gcg att aag ggt tca	720
Lys Asn Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser	
145 150 155	
cct tcc aag ctg cgc cgc att cta gag atc aac tct tcg gcg ttg gag	768
Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu	
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acc ttg aag ttt gag ggc cgc gag ctt tct gat gag ctg gtg tgg gaa	816
Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu	
175 180 185 190	
cgc att cat gca acc aag gcc gct gac ctg gcg tct ttg gtg tac acc	864
Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr	
195 200 205	
tct ggc aca act ggt agg ccg aag ggc tgc gag ttg tcc cac tac cac	912
Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His	
210 215 220	
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Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile	
225 230 235	
gcg atg cca ggt tca agg ttg ctc acc ttc ctt cct ttg gcg cac gtt	1008
Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val	
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ctt gct cgc gca gtg cac ttg gcc ttc gct gtc acc ggt gca acc cag	1056
Leu Ala Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln	
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tcc cac tgg tct gat ttc agc acc ctt act ttg gaa ctg cag cgt tcc	1104
Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser	
275 280 285	
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Arg Pro Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg	
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Asn Ala Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile	

Glu Ile Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser
560 565 570

gag gcg atc aag cgg ttc tac atc ctt gat cgc gac ctg acc gag gaa 2016
Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu
575 580 585 590

gcc gac gag ctg acc cca acg ctg aag gtc aag cgc aac gtt gtt gtt 2064
Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val
595 600 605

cgc cgt tac gca gac gcc atc gac cac atc tac aac cga tgagtaaac 2113
Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
610 615

agagacccaa tttgattggg atggatcgac atggaccgc accgaagtcg gcgaagcacc 2173

aacacgcttc gctgtgggcg tgatggagga ttctgcctac attgcagcca ctggcacgga 2233

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35 40 45

Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu
50 55 60

Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly
65 70 75 80

Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu
85 90 95

Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser
100 105 110

Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala
115 120 125

Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn
130 135 140

Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser
145 150 155 160

Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu
165 170 175

Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp
 515 520 525
 Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser
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 Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile
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 Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala
 565 570 575
 Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp
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 595 600 605
 Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
 610 615

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